

Proposal
entitled

**The Role of the National Bison Range in the Long-Term Management of Federal
Bison Herds**

Submitted to

**The U.S. Department of the Interior, U.S. Geological Survey & the U.S. Fish and
Wildlife Service**

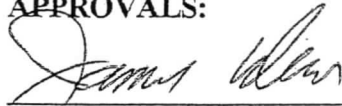
by

The Texas Agricultural Experiment Station
Texas A&M University System

Duration: 1 year

Amount Requested: \$28,000

APPROVALS:

 6/20/02

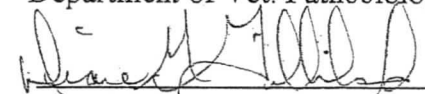
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PROJECT STATEMENT SHEET

PROJECT NUMBER:

Project Title: The Role of the National Bison Range in the Long-Term Management of Federal Bison Herds

SUBPROJECT TITLE:

FUNDING STATUS: FUNDED: \$ UNFUNDED: 0,0

SERVICE ISSUES:

CULTURAL RESOURCES TYPE CODE:

PACKAGE NUMBER

PROBLEM STATEMENT

Project Description: Bison are a unique and highly visible fauna of several western national wildlife refuges and national parks. Though many bison exist on private ranches, genetic diversity within private herds is being lost and limited by selection practices for particular traits and crossing bison with cattle. Public herds are viewed as keepers of the bison gene pool, and it is important for the future of this species that the remaining genetic diversity be preserved.

Gene flow between species whose members hybridize and subsequently backcross to one or both parental populations can result in the disintegration of genetic integrity and the loss of native genetic variation, thereby destroying the genetic structure of specific herds. Moreover, if the hybrids suffer from lower fertility, there are costs associated with this wasted reproductive effort. A number of bison herds have been identified that contain evidence of hybridization with domestic cattle and in some cases the hybridization can be traced back to one or more of the original foundation herds (Ward et. al. 1999). The majority of the animals that were used to established the federal herds came from pre 1900 private foundation herds and their hybrid status is not fully known. This is important due to the fact that interspecies hybrids have no taxonomic status which may present legal challenges regarding their protection, transportation and exchange with requests to petition bison.

The effect of hybridization events, past man-induced bottlenecks and animal relocations on the genetic integrity of federal bison is unknown. Population genetic parameters of each federal herd is needed to determine whether a strategy of genetic conservation is most appropriate at the herd level or among all the federal herds at the metapopulation level. The problem is very little genetic information is available regarding bison population structure and genetic integrity on parks and refuges. Federal managers charged with conserving bison germplasm must know

whether animals with hybrid backgrounds exist in these herds in order to prevent hybrid perpetuation. In addition, managers must be able to define the population structures or their herds in order to test the effect of various population sizes and removal strategies on genetic diversity. This information will clarify the best management strategies for the long-term preservation of bison germplasm.

This project relates to Service priority for the management and conservation of Fish & Wildlife Service bison herds that require genetic resource information (701 FW 8). None of the Fish & Wildlife Service herds have any baseline genetic information. Development of an Interior-wide bison genetics conservation strategy has been identified as a need by the Department of the Interior Bison Working Group. The USGS initiated a 4-year study with Texas A&M University on the genetics of all five NPS bison herds. A parallel study of the four Service herds is necessary to develop a Department of Interior-wide plan. The NPS study was initiated in 2000. The Fish & Wildlife Service has an immediate window to implement a sister study now so that the genetic information is available concurrently and a conservation strategy can be developed for all federal herds. The National Bison Range Complex believes this is a mission-critical project that should be completed now.

METHODS

Tissue samples will be collected using standard protocols (FTA cards for whole blood and paper envelopes for hair samples and post mortem tissue samples). DNA will be extracted by standard treatments.

Mitochondrial DNA analysis. DNA will be amplified using published procedures to test for maternal transmission of domestic cattle mitochondrial DNA (Ward et. al. 1999). In the event cattle mtDNA is detected, the complete mtDNA nucleotide sequence will be determined for the control region in order to establish the origin of any hybrid animal. In addition, a selected group of animals will be chosen and their mtDNA control region will be completely sequenced to examine nucleotide divergence and variability for populations structure analyses.

Nuclear DNA analysis. We have recently developed an Y chromosome molecular marker that will distinguish domestic cattle and bison paternal lineages (Ward et.al. 2001). All bison males will be tested for cattle Y chromosome specific markers. This analysis provides a companion analyses to mitochondrial DNA and is useful for detecting male transmission of cattle genes in the event of hybridization.

The nuclear genome will also be examined using a subset of over 300 microsatellite markers that were originally developed as part of the bovine genome project (Barendse, et.al. 1994; Bishop, et.al. 1994; Womack, 1993). We will select approximately 50 highly informative microsatellite markers that define chromosomal regions across the bison genome. This information will be used to define the genetic structure of the herd. For example, these markers are extremely powerful for

detecting inbreeding, overall genetic variation, population substructuring and any unique genetic features (i.e., alleles) that may be present in individual herds.

In addition, a set of 14 microsatellite markers are available that have been well characterized in bison for parentage testing and the construction of reverse pedigree analysis. Alleles at each of these microsatellite markers have been sequenced and we have successfully used these markers in the past to determine parentage in bison (Schnabel, et.al. 2001). This information will be used to develop the necessary statistical procedures to produce reverse pedigrees, if needed, and for the development of an interactive model to predict the long-term consequences of various management plans such as culling practices and the relocation of animals.

All microsatellite analyses have been optimized for multiplex loci detection with an Applied Biosystems automated DNA sequencer / genotyper allowing for very rapid data collection.

Desired Products: Information and data on the genetic status of the National Bison Range bison herd for inclusion in the Department of Interior genetic model for long-term management of bison genetic integrity.

Technical Assistance:

- 1) Store and archive all DNA samples on FTA cards (600 samples).
- 2) Process all samples for mtDNA testing for genetic purity to determine the presence of bovine genes (12 genes).
- 3) Process all samples for domestic cattle Y chromosomes.
- 4) Process at least 20% of samples for nuclear DNA testing (50 genes) for population parameters, relatedness within herd and among other federal herds.

MATERIALS

- 1) Electronic database established illustrating samples listed by individuals tag number, number of DNA samples, quality of DNA sample (good, fair, poor), and type of DNA sample (hair or blood stock).
- 2) Final report of mitochondrial DNA testing describing techniques, results and discussion of suspected hybrid individuals and recommendations for management.
- 3) Final report of nuclear DNA testing describing techniques, results and discussion of population genetic structure, relatedness among herd individuals, suspected hybrid individuals, degree of genetic variation, degree of heterozygosity and how that is reflected in the breeding structure of the herd, and recommendations for management.

These products will be used by refuge management to best determine management strategies that will not further perpetuate hybrid individuals, will maximize the long-term preservation of bison germplasm, and that will allow for removal of surplus bison that does not result in loss of genetic variation. Other Project Leaders will be able to contact National Bison Range for technical assistance in gaining this type of information. Ecological Services may need this information if the petition to list bison is ever reviewed. Finally, National Bison Range Project Leader can use this information to communicate and collaborate with National Park Service in developing an Interior-wide plan for the long-term conservation of bison.

Project Officer: Dr. Peter Gogan, Northern Rocky Mountain Science Center, Montana State University, Bozeman, MT 59717; 406/994-6989; fax 406/994-7085; pgogan@montana.edu

Funding Needs: National Bison Range requests **\$28,000** for genetic analysis of this bison herd.

6mo tech time stipend = \$6,495

Materials and supplies = \$4,353

MtDNA and nuclear DNA genotyping = \$11,500

Travel to collect samples and meet with USF&W personnel = \$2,000

15%overhead = \$3,652

Total for project = \$28,000

Travel: Travel support is requested to collect DNA samples, consult with and make contact with NPS personnel and attend scientific meetings to present research results.

Materials and Supplies: Laboratory supplies include DNA sequencing kits and genotyping supplies, synthetic oligonucleotides, disposable labware and chemical reagents for DNA isolation, purification and quantification.

Texas Agriculture Experiment Station Contribution:

Provide staff and equipment for three days to insert individual id tags, draw DNA blood samples and take hair samples of calves, all yearlings and two year olds, and all remaining cows, and return to Texas A&M University. Perform laboratory duties for all NBR samples for mtDNA determinations and nuclear gene analysis. Provide final report detailing the research findings.

USGS - Northern Rocky Mountain Science Center Contribution

(5% of Peter Gogan's time for a year)

Time Frame: Since this station has already obtained DNA samples and tagged every individual in the herd, only the testing and analysis are to be completed. Texas A&M University,

contracted by USGS, can complete the testing and provide recommendations within one year of obtaining funding.

Principal USGS Contact: Dr. Peter Gogan, 232B AGM Johnston Hall, Montana State University, Bozeman, MT 59717; 406/994-6989; fax 406/994-7085; pgogan@montana.edu.

Dr. Gogan is the Project Officer for the National Park Service bison genetics study. He coordinates closely with the Principal Investigator, Dr. James Derr. Dr. Gogan will be able to incorporate the National Bison Range project into his oversight and help both entities work towards developing a long-term conservation genetics management plan for bison managed by the Department of the Interior.

Principal Investigator: Dr. James N. Derr, Genetics & Veterinary Pathobiology, Texas A&M University, College Station, TX 77843-4467; 979/862-4775; fax 979/845-9972; jderr@cvm.tamu.edu

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- Ward, T.J., L.C. Skow, D.S. Gallagher, R.D. Schnabel, C.E. Kolinda, Chad Nall, S.K. Davis, J.F. Taylor and J.N. Derr. 2000. Differential introgression of uniparentally-inherited markers in bison populations with hybrid ancestries. *Animal genetics* 32:89-91.

EVALUATION CRITERIA

Significance: Bison are a highly unique and highly visible fauna of several western national parks that are greatly appreciated by the US public. Bison have also been identified as significant components of the ecosystem that influence soil processes, rates and amounts of nutrient cycling, and the amounts of nitrogen readily available to plants. The enabling legislation of several of the parks prioritizes wildlife and bison are listed high in park resource management plans. This proposal addresses BRD, BIN Nos. NPS-4, and NPS-5. NPS policy and guidelines specifically call for preservation of genetic resources and management of types as close as possible to the original, indigenous subspecies, or race (USDI, NPS 1988).

Severity: All aspects of bison management in federal herds are extremely controversial. Bison management is currently considered one of, if not the most controversial management topic within the Department of Interior. Recent management plans in Grand Teton, Yellowstone, and the other target parks all call for periodic herd reductions, albeit opportunistic removals of migrating bison from Yellowstone NP. Since some herd ceiling will be set for all populations, information on ways to maintain genetic resources with smaller populations is essential. In addition, defining herds that contain evidence of hybridization with domestic cattle is essential for the long-term conservation of this species.

Feasibility: The problem is well-defined and logistics, lab techniques, and current DNA technology make it feasible. This same study would not have been as successful even 10 years ago, considering the exponential rate of development of new technology in genetics.

Problem Resolution: Problem can be resolved with this 1-year study. A new genetics management plan should result for each of the target populations.

Transferability: The information will be directly applicable to the large number of bison herds on other federal, state, or private lands in the western and midwest US. Appropriate management of genetics and conservation of genetics is a common problem to the many small, isolated herds of bison.

Cost Effectiveness: Costs are realistic and informed. The NPS contract held by the PI and reduced overhead costs (15% as opposed to the typical 45.5%) granted by The Texas Agriculture Experiment Station will contribute to the overall resolution of the problem.